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Objective:

- Seeking a challenging position in bioinformatics, computational biology, genomics, environmental genomics, microbiology or related discipline.

Research Interests:

- Information theory based DNA binding site models; Microbial genomic diversity and evolution, comparative genomics; Environmental genomics of bacteria and phages; Evolutionary analysis of genes, proteins or genomes; Z curve based genomic analysis; Nucleotide and protein sequence analysis; Genomic data mining.

Current Research:

- T7-like promoter models: Using molecular information theory a total of ten promoter models were created for T7 group phages. These models can be used to identify new T7-like promoters. Phylogenetic analysis shows that the promoters have evolved differently from their polymerases;
- T7-like promoter containing regions in microbial genomes: The T7-like promoter models were used to scan more than 30 enterobacterial genomic sequences. More than 30 strong T7-like promoters were identified, within which 12 clusters of tandem T7-like promoters were found to be located within a novel group of prophage-like islands in nine enteropathogens, suggesting that these islands could be involved in pathogenicity;
- Large scale microbial genome scanning with the 10 T7-like promoter models. More than 200 bacterial genomes and 400 viral genomes were scanned with the 10 models, and more than 100 strong T7-like promoters were found. Some of the promoters and the corresponding flanking regions will be investigated in detail;
- Evolution of T7-like phages and their transcription systems: The evolution of the T7-like transcription systems, which consist of a T7-like RNAP and a set of conserved T7-like promoters, was studied by comparing with the evolution of phages, which was inferred based on the phylogenetic analysis of a set of orthologs shared by different phages;
- Information theory based models for Shine-Dalgarno (SD) sequences and RNase III recognition sites in the T7 group phages and their host genomes. The results show that the excess information at T7-like promoters can be explained by the takeover pressure, which is defined as the ratio between information contents of phage SD and corresponding host SD;
- Development and refinement of information theory based Fur binding site models, and comparative analysis of different Fur models.

Education:

- Sep 1991 - July 1995, B.S., Major in Freshwater Fishery, Southwest Agricultural University, Chongqing, China.
- Sep 1995 - Feb 2001, Ph.D., major in molecular biology, Shanghai Institute of Biochemistry and National Center for Gene Research, Chinese Academy of Sciences, Shanghai, China.
Prof. Guofan Hong,
Work on rice genome mapping, sequencing and analysis.
Ph.D. thesis:
Sequence-ready contig map construction and sequence analysis of a 1.8 Mb region close to the distal telomere of rice chromosome 4.

Brief Chronology of Employment:

- Feb 2001 - Oct 2001, Research Fellow, National Center for Gene Research, Chinese Academy of Sciences, Shanghai, China
Work on rice genome mapping, sequencing and analysis.
Job duties include:
Sequence-ready contig map construction; BAC clone sequencing, sequence assembly and gap filling; Genome sequence annotation and analysis; Discuss projects with the director; Design and conduct experimental work, and discuss with the director; Obtain information and knowledge of interest from the literature; Conduct sequence analysis using online available programs; Make a clear record of both experimental and computational work; Participate in lab meetings; Publish results in peer-reviewed journals;
- Nov 2001 - Present, Postdoctoral Fellow, Laboratory of Experimental and Computational Biology (LECB), (* Since Aug, 2005, LECB has been renamed to CCRNP—Center for Cancer Research Nanobiology Program *)
NCI-Frederick, CCR, NIH, Frederick, MD.
Work on molecular information theory.
Job duties include:
Discuss projects with advisor; Design and conduct experimental work, and discuss with advisor; Obtain information and knowledge of interest from the literature; Watch the databank for new sequence data of interest; Perform information theory analysis on sequences of interest; Conduct sequence analysis using other available programs; Make a clear record of both experimental and computational work, and maintain lab note books properly; Interpret results from both experimental and computational work, and formulate working hypotheses; Write up research reports monthly and discuss with advisor; Participate in lab meetings; Publish results of work in peer-reviewed journals; Attend and make presentations at national and international scientific meetings of interest; Fulfill training requirements of NIH and the lab, *e.g.*, the New Employee Safety Orientation and the NIH Ethics Training.

Presentations:

- Talk (by **Chen Z**): Information theory based DNA binding site models, 2006 June 9, at the SuperArray Biosciences Corporation: <http://www.superarray.com/>
- Talk (by **Chen Z**): Information theory analysis of T7-like phages, 2006 June 2, at the Biology Department of the Brookhaven National Laboratory: <http://www.biology.bnl.gov/>
- Talk (by **Chen Z**): Discovery of T7 Islands Using Information Theory Based T7-like Promoter Models, 2006 May 15, at the 2006 Texas, Evergreen Phage and Virus Genomics and Ecology Meeting: http://www.biochem.uthscsa.edu/~hs_lab/phage_meeting/
- Poster (by **Chen Z** and Schneider TD): Takeover Pressure Explains Excess Information at T7-like Promoters, 2006, May 12-15, at the 2006 Texas, Evergreen Phage and Virus Genomics and Ecology Meeting:
http://www.biochem.uthscsa.edu/~hs_lab/phage_meeting/
- Poster (by **Chen Z** and Schneider TD): Takeover Pressure Explains Excess Information at T7-like Promoters, 2005 Oct, at the 2005 NIH Research Festival:
<http://researchfestival.nih.gov/>
- Talk (by **Chen Z**): Information Theory Based T7-like Promoter Models: Evolution of T7-like Transcription Systems and Detection of a Novel Group of Genomic Islands Containing Tandem T7-like Promoters. 16th International Phage Biology Meeting:
<http://www.evergreen.edu/phage/meetings/2005meeting.htm>
- Poster (by **Chen Z** and Schneider TD): Comparative Analysis of T7-like Promoter Bearing Regions in Bacterial Genomes Reveals a Novel Group of Islands. TIGR's GSAC XVI:
<http://www.tigr.org/conf/gsac/>
- Poster (by **Chen Z** and Schneider TD): Comparative Analysis of T7-like Promoter Bearing Regions in Bacterial Genomes Reveals a Novel Group of Islands. 2004 NIH Research Festival: <http://researchfestival.nih.gov/festival04/default.htm>
- Poster (by **Lyakhov IG**, Chen Z and Schneider TD): A Novel Bacteriophage Lambda Cro Responsive Element in the oop RNA Promoter. 2004 NIH Research Festival:
<http://researchfestival.nih.gov/festival04/default.htm>
- Poster (by **Chen Z** and Schneider TD): Excess Information at T7-like Promoters and Classification of T7-like Phages. The Eighth Annual International Conference on Research in Computational Molecular Biology (RECOMB2004, <http://recomb04.sdsc.edu/>). Abstract (poster number K23) is available at:
<http://recomb04.sdsc.edu/cgi-admin/posterabstracts.cgi>
- Abstracts for the RGP Rice Genome Workshop:
<http://rgp.dna.affrc.go.jp/rgp/rgm7/Workshop.html>
<http://rgp.dna.affrc.go.jp/rgp/rgm6/rgm6ws.html>
- Abstracts for the International Plant & Animal Genome Conference (PAG):
<http://www.intl-pag.org/pag/7/abstracts/pag7189.html>
<http://www.intl-pag.org/pag/8/abstracts/pag8080.html>
<http://www.intl-pag.org/pag/9/abstracts/W52.01.html>

Professional Associations:

- International Society for Computational Biology: <http://www.iscb.org/>
- American Society for Microbiology: <http://www.asm.org/>

Manuscripts in Preparation:

- **Chen Z** and Schneider TD. **Takeover pressure explains excess information at T7-like promoters.** 2006, *in preparation*.
- **Chen Z** and Schneider TD. **Evolution of T7-like phages and their transcription systems.** 2006, *in preparation*.
- Lewis KA, **Chen Z**, Shultzaberger R, Lyakhov I, Zheng M, Doan B, Storz G and Schneider TD. **Discovery of Fur binding site clusters in *Escherichia coli* by an information theory model.** 2006, *in preparation*.

Publications:

- **Chen Z** and Schneider TD. **Comparative analysis of tandem T7-like promoter containing regions in enterobacterial genomes reveals a novel group of genetic islands.** *Nucleic Acids Res*, 2006, 34(4):1133-1147.
- **Chen Z** and Schneider TD. **Information theory based T7-like promoter models: classification of bacteriophages and differential evolution of promoters and their polymerases.** *Nucleic Acids Res*, 2005, 33(19):6172-6187.
- **Chen Z** and Schneider TD. **Excess information at T7-like promoters and classification of T7-like phages.** *RECOMB: Currents in Computational Molecular Biology*. 2004, 492-3.
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*Note: My name (Zehua Chen) in this paper was misspelled as “Zhehua Chen”.
- **Chen ZH**, Zhou B, Han B, Qian YM, Hong GF. **Structural Analysis of a Gene Cluster Encoding Two Cationic and Three Anionic Peroxidases from Rice Chromosome 4.** *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao* (Shanghai). 2001; 33(2):163-172.

- Zhou B, **Chen ZH**, Han B, Hong GF. **Identification and Structural Analysis of a class of Potentially Transposable Solo-LTR in Rice Genome.** *Sheng Wu Hua Xue Yu Sheng Wu Wu Li Xue Bao* (Shanghai). 2001;33(2):158-162.
- Liu ST, Chang WZ, Cao HM, Hu HL, **Chen ZH**, Ni FD, Lu HF, Hong GF. **A HU-like protein binds to specific sites within nod promoters of *Rhizobium leguminosarum*.** *J Biol Chem*. 1998 Aug 7;273(32):20568-74.

**References are available upon request!*

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